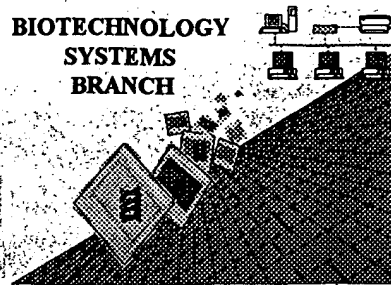


0590
12/9

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101003,674
Source: 01PE
Date Processed by STIC: 12/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 101003,674

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1 ☐ **Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,674

DATE: 12/14/2001

TIME: 11:10:29

Input Set : A:\Es.txt

Output Set: N:\CRF3\12142001\I003674.raw

**Does Not Comply
Corrected Diskette Needed**

4 <110> APPLICANT: Wolfe, M. Michael
 5 Tseng, Chi-Chuan
 6 Neville, Linda
 8 <120> TITLE OF INVENTION: Specific Antagonists for
 9 Glucose-Dependent Insulinotropic Polypeptide (GIP)
 12 <130> FILE REFERENCE: 50128/002002
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/003,674
 C--> 15 <141> CURRENT FILING DATE: 2001-10-23
 17 <150> PRIOR APPLICATION NUMBER: 60/032,329
 18 <151> PRIOR FILING DATE: 1996-12-03
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

-Misaligned amino numbering
throughout - see error
summary sheet #3.

ERRORED SEQUENCES

24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 30
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
 E--> 31 5 10 15 Ile His Gln Gln Asp Phe Val Asn
 E--> 32 Trp Leu Leu Ala Gln Lys 20 25 30
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 24
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Homo sapiens
 39 <400> SEQUENCE: 2
 40 Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys Ile His Gln Gln Asp Phe 1
 E--> 41 5 10 15 Val Asn Trp Leu Leu Ala Gln Lys
 E--> 42 20
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 15
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Homo sapiens
 49 <400> SEQUENCE: 3
 50 Lys Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1 5
 E--> 51 10 15
 53 <210> SEQ ID NO: 4
 54 <211> LENGTH: 9
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Homo sapiens or Rattus norvegicus
 58 <400> SEQUENCE: 4
 E--> 59 Ile Ser Asp Tyr Ser Ile Ala Met Asp 1 5
 61 <210> SEQ ID NO: 5
 62 <211> LENGTH: 21

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,674

DATE: 12/14/2001

TIME: 11:10:29

Input Set : A:\Es.txt

Output Set: N:\CRF3\12142001\I003674.raw

```

63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 5
67 Tyr Ser Ile Ala Met Asp Lys Ile His Gln Gln Asp Phe Val Asn Trp 1
E--> 68 5          10          15      Leu Leu Ala Gln Lys          20
70 <210> SEQ ID NO: 6
71 <211> LENGTH: 3
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens or Rattus norvegicus
75 <400> SEQUENCE: 6
E--> 76 Ile Ser Asp 1
78 <210> SEQ ID NO: 7
79 <211> LENGTH: 30
80 <212> TYPE: PRT
81 <213> ORGANISM: Rattus norvegicus
83 <400> SEQUENCE: 7
84 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 85 5          10          15      Ile Arg Gln Gln Asp Phe Val Asn
E--> 86 Trp Leu Leu Ala Gln Lys          20          25          30
88 <210> SEQ ID NO: 8
89 <211> LENGTH: 24
90 <212> TYPE: PRT
91 <213> ORGANISM: Rattus norvegicus
93 <400> SEQUENCE: 8
94 Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys Ile Arg Gln Gln Asp Phe 1
E--> 95 5          10          15      Val Asn Trp Leu Leu Ala Gln Lys
E--> 96 20
98 <210> SEQ ID NO: 9
99 <211> LENGTH: 15
100 <212> TYPE: PRT
101 <213> ORGANISM: Rattus norvegicus
103 <400> SEQUENCE: 9
104 Lys Ile Arg Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1          5
E--> 105 10          15
107 <210> SEQ ID NO: 10
108 <211> LENGTH: 21
109 <212> TYPE: PRT
110 <213> ORGANISM: Rattus norvegicus
112 <400> SEQUENCE: 10
113 Tyr Ser Ile Ala Met Asp Lys Ile Arg Gln Gln Asp Phe Val Asn Trp 1
E--> 114 5          10          15      Leu Leu Ala Gln Lys          20
116 <210> SEQ ID NO: 11
117 <211> LENGTH: 42
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 11
122 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 123 5          10          15      Ile His Gln Gln Asp Phe Val Asn
124 Trp Leu Leu Ala Gln Lys Gly Lys          20          25

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,674

DATE: 12/14/2001

TIME: 11:10:29

Input Set : A:\Es.txt

Output Set: N:\CRF3\12142001\I003674.raw

```

E--> 125 30      Lys Asn Asp Trp Lys His Asn Ile Thr Gln      35      40
      127 <210> SEQ ID NO: 12
      128 <211> LENGTH: 42
      129 <212> TYPE: PRT
      130 <213> ORGANISM: Rattus norvegicus
      132 <400> SEQUENCE: 12
      133 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 134 5      10      15      Ile Arg Gln Gln Asp Phe Val Asn
      135 Trp Leu Leu Ala Gln Lys Gly Lys      20      25
E--> 136 30      Lys Asn Asp Trp Lys His Asn Ile Thr Gln      35      40
      138 <210> SEQ ID NO: 13
      139 <211> LENGTH: 10
      140 <212> TYPE: PRT
      141 <213> ORGANISM: Homo sapiens or Rattus norvegicus
      143 <400> SEQUENCE: 13
E--> 144 Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1      5      10

```

VERIFICATION SUMMARY

DATE: 12/14/2001

PATENT APPLICATION: US/10/003,674

TIME: 11:10:30

Input Set : A:\Es.txt

Output Set: N:\CRF3\12142001\I003674.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:32 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:8 SEQ:1
L:41 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:42 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:42 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:8 SEQ:2
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:51 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:0 SEQ:3
L:59 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:4
L:68 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:5
L:76 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3 Found:0 SEQ:6
L:85 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:86 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:8 SEQ:7
L:95 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:96 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:96 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:8 SEQ:8
L:105 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:105 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:0 SEQ:9
L:114 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:10
L:123 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:42 Found:8 SEQ:11
L:134 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:136 M:252 E: No. of Seq. differs, <211>LENGTH:Input:42 Found:8 SEQ:12
L:144 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:13